GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on   January 16, 2003, 16:42:17 ; Search time 21.3573 Seconds
          (without alignments)
          58.517 Million cell updates/sec

Title: US-09-856-070-19
Perfect score: 65
Sequence: 1 KEELMLRLQDYEE 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_73:*
              1: pir1:*
              2: pir2:*
              3: pir3:*
              4: pir4:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length DB	ID			Description
1	65	100.0	581	I45889	2		ezrin - bovine
2	65	100.0	586	A34400	1		ezrin [validated]
3	65	100.0	630	T47177	2		hypothetical prote
4	62	95.4	586	B41129	1		ezrin - mouse
5	41	63.1	327	T42999	2		ethanolamine-phosp
6	41	63.1	365	T37720	2		ethanolamine-phosp
7	40	61.5	218	S75100	2		ABC transport prot
8	40	61.5	577	A41289	2		moesin - human
9	40	61.5	577	S39804	1		moesin (man)
10	40	61.5	583	A46127	2		radixin - human
11	40	61.5	583	S39905	1		radixin - pig
12	40	61.5	583	A41129	1		radixin - mouse
13	40	61.5	1263	T15496	2		hypothetical prote
14	39	60.0	250	H84112	2		hypothetical prote
15	39	60.0	405	B36440	2		alpha(1,3)-fucosyl
16	39	60.0	413	T31851	2		transposase tnI7 m
17	39	60.0	414	C90364	2		transposase ISC133
18	39	60.0	544	S75944	2		hypothetical prote
19	39	60.0	890	F75103	2		conserved hypothet
20	38	58.5	86	E96544	2		hypothetical prote
21	38	58.5	129	H84133	2		hypothetical prote
22	38	58.5	132	D90833	2		DNA packaging prot
23	38	58.5	132	E90900	2		probable DNA packa
24	38	58.5	145	F85690	2		hypothetical prote
25	38	58.5	150	G92449	2		hypothetical trans
26	38	58.5	150	AF2667	2		transcription requ
27	38	58.5	467	A49377	1		involucrin - mouse
28	38	58.5	632	I27499	2		hypothetical prote
29	38	58.5	756	T00367	2		hypothetical prote
30	38	58.5	1058	S65460	2		apolipoprotein B -
31	38	58.5	1400	I22644	2		hypothetical prote
32	37	56.9	94	S60798	2		M protein precurso
33	37	56.9	99	S71520	2		M protein type 18
34	37	56.9	111	T12857	2		hypothetical prote
35	37	56.9	160	G59101	2		hypothetical prote
36	37	56.9	250	A83244	2		conserved hypothet
37	37	56.9	281	I75416	2		hypothetical prote
38	37	56.9	303	A55592	1		cheA activity-modu
39	37	56.9	305	T64022	2		2,3-dihydroxybiphe
40	37	56.9	321	B82832	2		protein-export mem
41	37	56.9	337	A70364	1		conserved hypothet
42	37	56.9	338	C82254	2		conserved hypothet
43	37	56.9	454	S01592	2		fodrin alpha chain
44	37	56.9	622	I23804	2		hypothetical prote
45	37	56.9	1065	A64465	2		hypothetical prote

ALIGNMENTS

RESULT 1
I45889
ezrin - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 13-Aug-1999
C;Accession: I45889
R;Bergson, C.M.; Zhao, H.; Saijoh, K.; Duman, P.S.; Nestler, E.J.
Mol Cell Neurosci. 4, 64-73, 1993
A;Title: Ezrin and osteoectin, two proteins associated with cell shape and growth, a
A;Reference number: I45889
A;Accession: I45889
A;Status: Preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-581 <REP>
A;Cross-references: GB-M94364; NID:g285137; PIDN:AAA49513; PID:g289408
C;Superfamily: ezrin; protein 4.1 membrane binding domain homology
F;7-291/Domain: protein 4.1 membrane binding domain homology <Mll.

Query Match   100.0%;   Score 65;   DB 2;   Length 581;
Best Local Similarity   100.0%;   Pred. No. 0.0027;
Matches 13;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 KEELMLRLQDYEE 13
           |||||||||||||
Db   344 KEELMLRLQDYEE 356

RESULT 2
A34400
ezrin [validated] - human
N;Alternate names: cytovillin; p81 protein; villin 2
C;Species: Homo sapiens (man)
C;Date: 22-Jun-1990 #sequence_revision 14-Jul-1991 #text_change 08-Dec-2000
C;Accession: A34400; S09263; E61052
P;Turunen, O.; Winqvist, R.; Pakkanen, R.; Grzeschik, K.H.; Wahlstrom, T.; Vaheri, A
J.Biol.Chem. 264, 16727-16732, 1989
A;Title: Cytovillin, a microvillar Mr 75,000 protein. cDNA sequence, prokaryotic exp
A;Reference number: A34400; MUID:89380299; PMID:2674140
A;Accession: A34400
A;Molecule type: mRNA
A;Residues: 1-586 <CYO>
A;Cross-references: GB-J05021
R;Gould, K.L.; Bretscher, A.; Esch, F.S.; Hunter, T.
EMBO J. 8, 4133-4142, 1989
A;Title: cDNA cloning and sequencing of the protein-tyrosine kinase substrate, ezrin,
A;Reference number: S09263; MUID:90076135; PMID:2591371
A;Accession: S09263
A;Molecule type: mRNA
A;Residues: 2,586 <COO>
A;Cross-references: GB-X51521; NID:g31282; PIDN:CAA35893.1; PID:g31283

R:Hauw, G.; Rasmussen, H.H.; Van den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.;
Electrophoresis 11, 528-536, 1990
A:Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencing
A:Reference number: A61002; MUID:91031404; PMID:1699755
A:Accession: F61002
A:Molecule type: protein
A:Residues: 255, 263;194,'Q',196-199,'X',201,264 270 <BAU>
A:Note: it is not certain whether this material represents ezrin or radixin (see entry A
A:Note: this material corresponds to transformed epithelial amnion cell (AMA) database f
C:Comment: This protein is located in microvilli and is proposed to play a role in modul
C:Genetics:
A:Gene: CDH:VIL2
A:Cross reference: CDB:120489; OMIM:123900
A:Map position: 6q25-q26
C:Superfamily: ezrin; protein 4.1 membrane binding domain homology
C:Keywords: actin binding; cytoskeleton; membrane associated protein; phosphoprotein
F:2-586/Product: ezrin #status experimental <MAT>
F:7-291/Domain: protein 4.1 membrane binding domain homology <B4I>
F:553-586/Region: actin binding #status predicted
F:66/Binding site: phosphate (Ser) (covalent) #status predicted
F:214,299,432/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match   100.0%;   Score 65;   DB 1;   Length 586;
Best Local Similarity   100.0%;   Pred. No. 0.0029;
Matches 13;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 KEELMLRLQDYEE 13
             |||||||||||||
Db   344 KEELMLRLQDYEE 356

RESULT 3
T47177
hypothetical protein DKFZp762H157.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20 Apr 2000 #sequence_revision 28 Apr 2000 #text_change 02 Sep 2000
C:Accession: T47177
R:Bottenwaelder, R.; Obermaier, B.; Mewes, H.W.; Weil, H.; Wiemann, S.
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224477
A:Accession: T47177
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-630 <AAA>.
A:Cross-references: EMBL:AL162086
A:Experimental source: adult melanoma (MeWo cell line); clone DKFZp762H157
C:Genetics:
A:Note: DKFZp762H157.1
C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology

Query Match   100.0%;   Score 65;   DB 2;   Length 630;
Best Local Similarity   100.0%;   Pred. No. 0.003;
Matches 13;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 KEELMLRLQDYEE 13
             |||||||||||||
Db   188 KEELMLRLQDYEE 400

RESULT 4
B41129
ezrin - mouse
N:Alternate names: cytovillin; p81 protein; radixin; villin 2
C:Species: Mus musculus (house mouse)
C:Date: 03 Aug 1992 #sequence_revision 14 Jul 1994 #text_change 22 Jun 1999
C:Accession: B41129; C41129; A45501; B45501; S24200
R:Funayama, N.; Nagafuchi, A.; Sato, N.; Tsukita, S.; Tsukita, S.
J. Cell Biol. 115, 1039-1048, 1991
A:Title: Radixin is a novel member of the band 4.1 family.
A:Reference number: A41129; MUID:92044635; PMID:1955455
A:Accession: B41129
A:Molecule type: mRNA
A:Residues: 1-586 <FUN>.

A:Cross references: EMBL:X6667; NID:g508807; PIDN:CAA41088.1; PID:g508807
R:Egerton, M.; Burgess, W.H.; Chen, D.; Druker, B.J.; Hretscher, A.; Samelson, L.E.
J. Immunol. 149, 1847-1852, 1992
A:Title: Identification of ezrin as an 81-kDa tyrosine phosphorylated protein in T-ce
A:Reference number: A46501; MUID:92388649; PMID:1381889
A:Accession: C46501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 412-426 <EGE>
A:Experimental source: MRL lpr/lpr T-cells
A:Note: sequence extracted from NCBI backbone (NCBIP:112938)
A:Accession: A46501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 27-33,'E' <EG2>
A:Experimental source: MRL lpr/lpr T-cells
A:Note: sequence extracted from NCBI backbone (NCBIP:112936)
A:Accession: B46501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 55,57,148,'L',150,'G',152-155 <EG3>
A:Experimental source: MRL lpr/lpr T-cells
A:Note: sequence extracted from NCBI backbone (NCBIP:112940)
C:Comment: This protein is located in microvilli and is proposed to play a role in mo
C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
C:Keywords: actin binding; cytoskeleton; cytosol; membrane-associated protein; phosph
F:2-586/Product: ezrin #status predicted <MAT>
F:7-291/Domain: protein 4.1 membrane-binding domain homology <B4I>
F:553-586/Region: actin binding #status predicted
F:66/Binding site: phosphate (Ser) (covalent) #status predicted
F:214,299,332/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match   95.4%;   Score 62;   DB 1;   Length 586;
Best Local Similarity   92.3%;   Pred. No. 0.009;
Matches 12;   Conservative 1;   Mismatches 0;   Indels 0;   Gaps 0;

Qy   1 KEELMLRLQDYEE 13
             ||||||||||| ||
Db   344 KEELMLRLQDYEE 356

RESULT 5
T42999
ethanolamine phosphate cytidylyltransferase homolog - fission yeast (Schizosaccharomy
C:Species: Schizosaccharomyces pombe
C:Date: 11 Jan 2000 #sequence_revision 11 Jan 2000 #text_change 21 Jul 2000
C:Accession: T42999
R:Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: 217323; MUID:98162722; PMID:9501991
A:Accession: T42999
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-427 <YOS>
A:Cross-references: EMBL:D89199; NID:g1749605; PIDN:HAA13860.1; PID:g1749606
A:Experimental source: strain PR745

Query Match   63.1%;   Score 41;   DB 2;   Length 427;
Best Local Similarity   61.5%;   Pred. No. 19;
Matches 8;   Conservative 2;   Mismatches 3;   Indels 0;   Gaps 0;

Qy   1 KEELMLRLQDYEE 13
             |: |||| ||
Db   295 KQRVMLRRQHYEE 307

RESULT 6
T37720
ethanolamine phosphate cytidylyltransferase (EC 2.7.7.14) - fission yeast (Schizosacc
C:Species: Schizosaccharomyces pombe
C:Date: 03 Dec 1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T37720

R:Murphy, I.; Harris, D.; Harris, R.C.; Rajandream, M.A.; Rine, M.H.
submitted to the EMBL Data Library, August 1999
A;Reference number: 221739
A;Accession: T37720
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-365 <MURE>
A;Cross-references: EMBL:AH104730; PIDN:CAB52434.1; GSP:6ENG0666; SFW:SPAC15E1.05c
A;Experimental source: strain 972h-; cosmid c15E1
C;Genetics:
A;Gene: SPDB-SPAC15E1.05c
A;Map position: 1
A;Introns: 2;/1
C;Keywords: nucleotidyltransferase

Query Match   63.1%;   Score 41; DB 2;   Length 365;
Best Local Similarity 61.5%;   Pred. No. 21;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy   1 KEELMLRLQDYEE 13
        |: ||| | ||||
Db 333 KQRVMLRRQHYEE 345

RESULT 7
S75100
ABC transport protein - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sll0240
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 02-Feb-2001
C;Accession: S75100
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular Cyanobacterium Synechocystis
s.
A;Reference number: S74322, MUID:37061263; PMID:8606521
A;Accession: S75100
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-218 <KAN>
A;Cross-references: EMBL:D90916, CB:AKM000, NID:g1653434, PIDN:HAA10762.1; PID:D10803
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: short chain ATP binding cassette proteins. ATP binding cassette homology
C;Keywords: ATP; nucleotide binding; P-loop
F;17-210/Domain: ATP binding cassette homology <ABC>
F;34-41/Region: nucleotide binding motif A (P-loop)

Query Match   61.5%;   Score 40; DB 2; Length 218.
Best Local Similarity 72.7%;   Pred. No. 18;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy   1 KEELMLRLQDY 11
        |||| |||
Db 169 KEELITYLQDY 179

RESULT 8
A41289
moesin - human
N;Alternate names: membrane-organizing extension spike protein
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
C;Accession: A41289
R;Lankes, W.T.; Furthmayr, H.
Proc Natl. Acad. Sci. U.S.A. 88, 8297-8301, 1991
A;Title: Moesin: a member of the protein 4.1-talin-ezrin family of proteins.
A;Reference number: A41289; MUID:92020840; PMID:1924285
A;Accession: A41289
A;Molecule type: mRNA
A;Residues: 1-577 <LAN>
A;Cross-references GB:M69066; NID:g188625; PIDN:AAA36322.1; PID:g188625

C;Comment: Moesin is proposed to be involved in linking the cytoskeleton to the plasm
C;Genetics:
A;Gene: GDB:MSN
A;Cross-references: GDB:136819; OMIM:309845
A;Map position: Xq11.2-Xq12
C;Superfamily: ezrin; protein 4.1 membrane-binding domain homology
C;Keywords: actin binding, cytoskeleton, membrane protein
F;7-577/product: moesin #status predicted <MAT>
F;7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
F;544-577/Region: actin binding #status predicted

Query Match   61.5%;   Score 40; DB 1;   Length 577;
Best Local Similarity 69.2%;   Pred. No. 50;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy   1 KEELMLRLQDYEE 13
        ||||| ||: ||
Db 344 KEELMERLKQIEE 356

RESULT 9
S39804
moesin - pig
N;Alternate names: membrane organizing extension spike protein
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
C;Accession: S39804
R;Lankes, W.T.; Schwartz-Albiez, R.; Furthmayr, H.
Biochim. Biophys. Acta 1216, 479-482, 1993
A;Title: Cloning and sequencing of porcine moesin and radixin cDNA and identification
A;Reference number: S39804, MUID:94062743; PMID:8286231
A;Accession: S39804
A;Molecule type: mRNA
A;Residues: 1-577 <LAN>
A;Cross-references: EMBL:M86450; NID:g164581; PIDN:AAB02864.1; PID:q164582
C;Comment: Moesin is proposed to be involved in linking the cytoskeleton to the plasm
C;Superfamily: ezrin; protein 4.1 membrane-binding domain homology
C;Keywords: actin binding, cytoskeleton, membrane protein
F;7-577/product: moesin #status predicted <MAT>
F;7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
F;544-577/Region: actin binding #status predicted

Query Match   61.5%;   Score 40; DB 1;   Length 577;
Best Local Similarity 69.2%;   Pred. No. 50;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy   1 KEELMLRLQDYEE 13
        ||||| ||: ||
Db 344 KEELMERLKQIEE 356

RESULT 10
A46127
radixin - human
C;Species: Homo sapiens (man)
C;Date: 2-Sep-1994 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
C;Accession: A46127
R;Wilgenbus, K.K.; Milatovich, A.; Francke, U.; Furthmayr, H.
Genomics 16, 199-206, 1993
A;Title: Molecular cloning, cDNA sequence, and chromosomal assignment of the human ra
A;Reference number: A46127; MUID:93252378; PMID:8486357
A;Accession: A46127
A;Molecule type: mRNA
A;Residues: 1-583 <WIL>
A;Cross-references GB:L02320; NID:g307365; PIDN:AAA51541.1; PID:g307366
A;Note: sequence extracted from NCBI backbone (NCBIP:131181; NCBIP:131182)
C;Genetics:
C;Comment: Radixin is a capping protein for the barbed end of actin filaments and it
A;Gene: GDB:RDX
A;Cross-references: GDB:136278, OMIM:179410
A;Map position: 11q23-11q23
C;Superfamily: ezrin; protein 4.1 membrane-binding domain homology
C;Keywords: actin binding, cytoskeleton

F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
F:470-477/Region: proline-rich
F:550-583/Region: actin binding #status predicted

Query Match   61.5%; Score 40; DB 1; Length 583;
Best Local Similarity 69.2%; Pred. No. 51;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KEELMLRLQDYEE 13
   |||| ||; ||
Db 344 KEELMERLKQIEE 356

RESULT 11
S39805
radixin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 19-May-1994 #sequence_revision 14-Jul-1994 #text_change 22-Jun-1999
C:Accession: S39805
R:Lankes, W.T., Schwartz-Albiez, R., Furthmayr, H.
Biochim. Biophys. Acta 1216, 479-482, 1993
A:Title: Cloning and sequencing of porcine moesin and radixin cDNA and identification of
A:Reference number: S39804; MUID:94092743; PMID:8268231
A:Accession: S39805
A:Molecule type: mRNA
A:Residues: 1-583 <LAN>
A:Cross-references: GB:M86444; EMBL:M86444; NID:g164585; PIDN:AAB02865.1; PID:g164586
C:Comment: Radixin is a capping protein for the barbed end of actin filaments and it is
C:Superfamily: ezrin; protein 4.1 membrane binding domain homology
C:Keywords: actin binding; cytoskeleton
F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
F:470-477/Region: proline-rich
F:550-583/Region: actin binding #status predicted

Query Match   61.5%; Score 40; DB 1; Length 583;
Best Local Similarity 69.2%; Pred. No. 51;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KEELMLRLQDYEE 13
   |||| ||; ||
Db 344 KEELMERLKQIEE 356

RESULT 12
A41129
radixin - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Aug-1992 #sequence_revision 14-Jul-1994 #text_change 05-Sep-1997
C:Accession: A41129; S24201
R:Funayama, N., Nagafuchi, A., Sato, N., Tsukita, S., Tsukita, S.
J. Cell Biol. 115, 1039-1048, 1991
A:Title: Radixin is a novel member of the band 4.1 family.
A:Reference number: A41129; MUID:92064635; PMID:1955455
A:Accession: A41129
A:Molecule type: mRNA
A:Residues: 1-583 <FUN>
A:Cross-references: EMBL:X60672; NID:g1034049; PID:g1334260
A:Note: part of this sequence was confirmed by protein sequencing
C:Comment: Radixin is a capping protein for the barbed end of actin filaments and it is
C:Superfamily: ezrin; protein 4.1 membrane-binding domain homology
C:Keywords: actin binding; cytoskeleton
F:7-291/Domain: protein 4.1 membrane-binding domain homology <B41>
F:470-477/Region: proline-rich
F:550-583/Region: actin binding #status predicted

Query Match   61.5%; Score 40; DB 1; Length 583;
Best Local Similarity 69.2%; Pred. No. 51;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KEELMLRLQDYEE 14
   |||| ||; ||
Db 344 KEELMERLRQIEE 356

RESULT 13
T15496
hypothetical protein C14F5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15496
R:Minx, P.
submitted to the EMBL Data Library, June 1995
A:Description: the sequence of C. elegans cosmid C14F5.
A:Reference number: z18361
A:Accession: T15496
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-1263 <MIN>
A:Cross-references: EMBL:U29082; NID:g861384; PIDN:AAA68402.1; PID:g861384
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:C14F5.3
A:Introns: 21/3, 34/2, 74/2, 252/2, 84/2, 42, 42, 292, 4141, 14, 47, 112

Query Match   61.5%; Score 40; DB 2; Length 1264;
Best Local Similarity 61.5%; Pred. No. 1.1e-02;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KEELMLRLQDYEE 13
   ::|| :||||||
Db 909 EEEQHAKIQDYEE 921

RESULT 14
H84212
hypothetical protein Vng0546c [imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: H84212
P:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lacky,
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Ja
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: A84160; MUID:20504483; PMID:11016950
A:Accession: H84212
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250 <STO>
A:Cross-references GB:AE004437. NID:g16586146. PIDN:AAG19668.1; GSPDB:GN00138
C:Genetics:
A:Gene: VNG0546C
C:Superfamily: 3-isopropylmalate dehydratase leuD chain

Query Match   60.0%; Score 39; DB 2; Length 250;
Best Local Similarity 66.7%; Pred. No. 31;
 Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KEELMLRLQDYEE 13
   ||: ||| ||
Db 226 EEVVSRLQDMEE 237

RESULT 15
B36340
alpha(1,3)-fucosyltransferase (EC 2.4.1.-) 4 precursor [validated] - human
N:Alternate names: CD15; ELAM-1 ligand fucosyltransferase (ELFT); FCT3A; FUC-IIV; myc
C:Species: Homo sapiens (man)
C:Date: 29-Apr-2000 #sequence_revision 29-Apr-2000 #text_change 28-Apr-2000
C:Accession: B36340; A36340; A40976; A41292
R:Goelz, S.E.; Hession, C.; Goff, D.; Griffiths, B.; Lizard, R.; Newman, B.; Chi-Rosso
Cell 63, 1349-1356, 1990
A:Title: ELFT: a gene that directs the expression of an ELAM-1 ligand.
A:Reference number: A36340; MUID:91084863; PMID:1702014
A:Accession: B36340

A;Molecule type: mRNA
A;Residues: 1-405, 'GOE1.
A;Cross-references: GB:M58597; NID:g182070; PIDN:AAA:417. l; PID:g182070
A;Accession: A36340
A;Molecule type: mRNA
A;Residues: 'MRPLWGAAPKPSGAGWEKEWAEAPAGEAPAGAWSGRLGPGP','SGPKGRAVPGWASWPAHLALAAKPARHLGGAGQ
A;Cross-references: GB:M58597; NID:g182070; PIDN:AAA63173.1, PID:q182071
A;Note: the codon used as an initiator for this translation is not in a good context for
R;Lowe, J.B.; Kukowska-Latallo, J.F.; Nair, R.P.; Larsen, R.D.; Marks, R.M.; Macher, H.A
J. Biol. Chem. 266, 17467-17477, 1991
A;Title: Molecular cloning of a human fucosyltransferase gene that determines expression
A;Reference number: A40976; MUID:9137370; PMID:1716630
A;Accession: A40976
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-86,'P',88-405 <LOW>
A;Cross-references: GB:M65030; NID:g182791; PIDN:AAA92977.1, PID:g236720
R;Kumar, R.; Potvin, B.; Muller, W.A.; Stanley, P.
J. Biol. Chem. 266, 21777-21783, 1991
A;Title: Cloning of a human alpha(1,3)-fucosyltransferase gene that encodes ELFT but doe
A;Reference number: A41202; MUID:92042084; PMID:1718983
A;Accession: A41202
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-240,'D',242-400 <KCM>
A;Cross-references: GB:S65161; NID:g239005; PIDN:AAB20349.1, PID:q239006
C;Genetics:
A;Gene: GDB:FUT4; CD15; FCT3A; FUC-TIV
A;Cross-references: GDB:131563; OMIM:104230
A;Map position: 11q21-11q21
C;Superfamily: galactoside 3(4)-L-fucosyltransferase
C;Keywords: glycoprotein; glycosyltransferase; hexosyltransferase
F;1-48/Domain: signal sequence #status predicted <SIG>
F;49-405/Product: alpha(1,3)-fucosyltransferase 4 #status predicted <MAT>
F;91,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match   60.0%;   Score 39;   DB 2;   Length 405,
Best Local Similarity   66.7%;   Pred. No. 52;
Matches   8;   Conservative   2;   Mismatches   2;   Indels   0,   Gaps   0;

Qy   2 EELMLRLQDYEE 13
           ||: ||: |||
Db   136 EEVDLRVLDYEE 147

Search completed: January 16, 2003, 16:57.50
Job time : 22.3571 secs